

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar

(ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 12

(i) CORRESPONDENCE ADDRESS:

v) CORRESPONDENCE INFORMATION

(A) ADDRESSEE: Brown, Martin, Haller & McClain
(B) STREET: 1660 Union Street
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92101-2926

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

1) CURRENT APPLICATION:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

11) PRIOR ART/RELEVANT
(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:

(iii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 6869-402A

(iv) TELECOMMUNICATION INFORMATION:

X) TELECOMMUNICATIONS
(A) TELEPHONE: 619-238-0999
(B) TELEFAX: 619-238-0062
(C) TELEEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

-) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i) MOLECULE TYPE: Genomic DNA

(ii) MOLECULE TYPE: GENETIC

(iii) HYPOTHETICAL
(iii) ANTI-SENSE: NO

- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| GAATTCATCA | TTTTCANGT | CCTCAAGTGG | ATGTTTCTCA | TTTNCCATGA | TTTTAAGTTT | 60 |
| TCTCGCCATA | TCCTGGTCC | TACAGTGTGC | ATTTCTCCAT | TTNCACGTT | TTNCAGTGAT | 120 |
| TTCGTCAATT | TCAAGTCCTC | AAGTGGATGT | TTCTCATTN | CCATGAATT | CAGTTTCTN | 180 |
| GCCATATTCC | ACGTCCTACA | GNGGACATT | CTAAATTNC | CACCTTTTC | AGTTTCCTC | 240 |
| GCCATATTTC | ACGTCCTAAA | ATGTGTATT | CTCGTTNCC | GTGATTTCA | GTGATTTCA | 300 |
| CAGATTCCAG | GTCCTATAAT | GTGCATTCT | CATTTNNCAC | GTGATTTCA | GATTCGTCA | 360 |
| TTTTTCAAG | TCGGCAAGTG | GATGTTCTC | ATTNCAGT | TTTNCAGT | TTCTTGNAAT | 420 |
| ATTCCATGTC | CTACAATGAT | CATTTTAAT | TTTCCACCT | TTCATTTTC | CACGCCATAT | 480 |
| TTCATGTCC | AAAGTGTATA | TTTCTCCTT | TCCCGGATT | TCAGTTTCT | CGCCATATTC | 540 |
| CAGGTCCCTAC | AGTGTGCATT | CCTCATT | CACCTTTTC | ACTGATTTG | TCATTTTCA | 600 |
| AGTCGTCAAC | TGGATCTTC | TAATTTCCA | TGATTTCA | TTATCTTGT | ATATTCCATG | 660 |
| TCCTACAGTG | GACATTCTA | AATTTCCAA | CTTTTCA | TTTCTCGAC | ATATTGACG | 720 |
| TGCTAAAGTG | TGTATTCTT | ATTTCCGTG | ATTTTCAGT | TTCTCGCCAT | ATTCCAGGTC | 780 |
| CTAATAGTGT | GCATTCTCA | TTTTCACGT | TTTCAGTGA | TTCGTCATT | TTTCCAGTT | 840 |
| GTCAAGGGGA | TGTTTCTCAT | TTTCCATGAG | TGTCAGTTT | CTTGCTATAT | TCCATGTCCT | 900 |
| ACAGTGACAT | TTCTAAATAT | TATACCTTT | TCAGTTTTC | TCACCATATT | TCACGTCTA | 960 |
| AAGTATATAT | TTCTCATT | CCCTGATT | CAGTTTCTT | GCCATATTCC | AGGTCTAC | 1020 |
| GTGTGCATT | CTCATT | ACGTTTCA | GTAATTCTT | CATTTTTAA | GCCCTCAAAT | 1080 |
| GGATGTTCT | CATTTCCAT | GATTTCA | TTTCTTGCA | TATACCATGT | CCTACAGTGG | 1140 |
| ACATTCTAA | ATTATCCACC | TTTTCA | TTTCATCGGC | ACATTTCA | TCCTAAAGTG | 1200 |
| TGTATTCTA | ATTTCA | ATTTCA | TTCTCGCCAT | ATTCCAGGAC | CTACAGTGTG | 1260 |
| CATTCTCAT | TTTCACGT | TTTCAGTGA | TTC | | | 1293 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1044 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGGCCTATGG | TGAAAAGGA | AATATCTTCC | CCTGAAA | AGACAGAAGG | ATTCTCAGAA | 60 |
| TCTTATTG | GATGTGCGCC | CCTCAACTAA | CAGTGTGAA | GCTTTCTT | GATAGAGCAG | 120 |
| TTTGAAACA | CTCTTTTGT | AAAATCTGCA | AGAGGATATT | TGGATAGCTT | TGAGGATTTC | 180 |
| CGTTGGAAAC | GGGATTGTCT | TCATATAAAC | CCTAGACAGA | AGCATTCTCA | GAAGCTTCAT | 240 |
| TGGGATGTT | CAGTTGAAGT | CACAGTGTG | AACAGTCCCC | TTTCATAGAG | CAGGTTGAA | 300 |
| ACACTCTTT | TTGTAGTATC | TGGAAGTGG | CATTTGGAGC | GATCTCAGGA | CTGCGGTGAA | 360 |
| AAAGGAAATA | TCTTCCAATA | AAAGCTAGAT | AGAGGCAATG | TCAGAAACCT | TTTCATGAT | 420 |
| GTATCTACTC | AGCTAACAGA | GTTAACCTT | CCTTGAGAG | AGCAGTTTG | AAACACTCTT | 480 |
| TTTGTGGAAT | CTGCAAGTGG | ATATTGTCT | AGCTTGAGG | ATTTCGTTGG | GAAACGGGAT | 540 |
| TACATATAAA | AAGCAGACAG | CAGCATTCCC | AGAAACTTCT | TTGTGATGTT | TGCATTCAAG | 600 |
| TCACAGAGTT | GAACATTCCC | TTTCATAGAG | CAGGTTGAA | ACACACTTTT | TGATGTATCT | 660 |
| GGATGTGGAC | ATTTCAGCG | CTTTCAGGCC | TAAGGTGAAA | AGGAAATATC | TTCCCCTGAA | 720 |

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| AACTAGACAG | AAGCATTCTC | AGAAACTTAT | TTGTGATGTG | CGCCCTCAAC | TAACAGTGT | 780 |
| GAAGCTTTCT | TTTGATAGAG | GCAGTTTGA | AACACTCTT | TGTGGAATCT | GCAAGTGGAT | 840 |
| ATTTGTCTAG | CTTGAGGAT | TTCTTGGAA | ACGGGATTAC | ATATAAAAAG | CAGACAGCAG | 900 |
| CATTCCCAGA | ATCTTGTGTTG | TGATGTTGC | ATTCAAGTCA | CAGAGTTGAA | CATTCCCTTT | 960 |
| CAGAGAGCAG | GTGGAACAC | TCTTTTATA | GTATCTGGAT | GTGGACATT | GGAGCGCTTT | 1020 |
| CAGGGGGGAT | CCTCTAGAAAT | TCCT | | | | 1044 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| CTGCAGCTGG | GGGTCTCCAA | TCAGGCAGGG | GCCCCTTACT | ACTCAGATGG | GGTGGCCGAG | 60 |
| TAGGGGAAGG | GGGTGCAGGC | TGCATGAGTG | GACACAGCTG | TAGGACTACC | TGGGGGCTGT | 120 |
| GGATCTATGG | GGGTGGGGAG | AAGCCCAGTG | ACAGTGCCTA | GAAGAGACAA | GGTGGCCTGA | 180 |
| GAGGGTCTGA | GGAACATAGA | GCTGGCCATG | TTGGGGCCAG | GTCTCAAGCA | GGAAGTGAGG | 240 |
| AATGGGACAG | GCTTGAGGAT | ACTCTACTCA | GTAGCCAGGA | TAGCAAGGAG | GGCTTGGGGT | 300 |
| TGCTATCCTG | GGGTCAACC | CCCCAGGTTG | AAGGCCCTGG | GGGAGATGGT | CCCAGGACAT | 360 |
| ATTACAATGG | ACACAGGAGG | TTGGGACACC | TGGAGTCACC | AAACAAAACC | ATGCCAAGAG | 420 |
| AGACCATGAG | TAGGGGTGTC | CAGTCCAGCC | CTCTGACTGA | GCTGCATTGT | TCAAATCCAA | 480 |
| AGGGCCCTG | CTGCCACCTA | GTGGCTGATG | GCATCCACAT | GACCCTGGGC | CACACGCGTT | 540 |
| TAGGGTCTCT | GTGAAGACCA | AGATCCTTGT | TACATTGAAC | GACTCCTAAA | TGAGCAGAGA | 600 |
| TTTCCACCTA | TTCGAAACAA | TCACATAAAA | TCCATCCTGG | AAAAGCCTG | GGGGATGGCA | 660 |
| CTAAGGCTAG | GGATAGGGTG | GGATGAAGAT | TATAGTTACA | GTAAGGGTT | TAGGGTTAGG | 720 |
| GATCAACGTT | GGTTAGGAGT | TAGGGATACA | GTAGGGTACC | GGTAGGGTTA | GGGGTTAGGG | 780 |
| TTAGGGTTA | GGGTTAGGGT | TAGGGTTAGG | GTTAGGGTTA | GGGGTTAGGG | GTTAGGGTTA | 840 |
| GGGTTAGGTT | TTGGGGTGGC | GTATTGGT | CTTATACGCT | GTGTTCCACT | GGCAATGAAA | 900 |
| AGAGTTCTTG | TTTTCCCTTC | AGCAATTGT | CATTTTAAA | AGAGTTTAGC | AATTCTAAC | 960 |
| GATATAGACC | AGCTGTGCTA | TCTCATTGTG | GTTTTCAATT | GTAACCACAT | TGTGGTTCA | 1020 |
| ATGTGTTAC | TTGCCATCTG | TAGATCTTCT | TTGCGTGAGG | TGTCTGTTCA | GATGTGTGTG | 1080 |
| CATTCTTGN | NTTNGGCTG | TTAACTTAT | TGTTTAGTT | TAATAATT | TTATATATT | 1140 |
| GAAGACAAAT | CTTCTCAGA | TGTGTATTTG | CAAATATTC | TTCAATATGA | GGCTTGCTTT | 1200 |
| TGTCTAAC | AAGGTCTCTT | CAGAGATAAC | TTAAATATAA | GAAATCCACA | CTGTCACCTC | 1260 |
| TTTGTGTAT | ATCTACCTT | TGTGTCATT | GTAAAATT | ATTACCAAAAC | CCAAAGGCAG | 1320 |
| ATAGCTTTTC | TTCTTATTGTT | TCTCTAGAA | ATTGTATAG | TTTGCATT | TTAGTGTAAAG | 1380 |
| GATGATTGG | AGTGATTATT | TGTGTAAGTT | GTAAAGTTT | CGTCTATATC | CATATCATT | 1440 |
| CTTATGGTT | CCAATTAATC | GTTCCCTCAC | TATTTTG | AAAGACACAG | GATAGTGGC | 1500 |
| TTTGTAGAG | TAGATAGGTA | GCTAGACATG | AACAGGAGGG | GGCCTCTGG | AAAAGGGAAA | 1560 |
| GCTCTGGGAAG | GCTCACCTGG | AGGACCACCA | AAAATTACA | TATTAGTAGC | ATCTCTAGTG | 1620 |
| CTGGAGTGGA | TGGCACTTG | TCAATTGTGG | GTAGGAGGG | AAAGAGGTCC | TATGCAGAAA | 1680 |
| GAAACTCCCT | AGAACTCCTC | TGAAGATGCC | CCAATCATTC | ACTCTGCAAT | AAAATGTCA | 1740 |
| GAATATTGCT | AGCTACATGC | TGATAAGGNN | AAAGGGGACA | TTCTTAAGTG | AAACCTGGCA | 1800 |
| CCATAAGTAC | AGATTAGGGC | AGAGAAGGAC | ATTCAAAAGA | GGCAGGGCGCA | GTAGGTACAA | 1860 |
| ACGTGATCGC | TGTCACTGTG | CCTGGGATGG | CGGGAAAGGAG | GCTGGTGCCA | GAGTGGATT | 1920 |

GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
 GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
 TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG 2100
 GCTGTTAAT GCATCGCTCA GTCCCACCTCC TCCCTATTG TCTACAATAA ACTCTTACA 2160
 CTGTGTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCCTTTGG TGAAAATGTT 2220
 TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
 TTGAATTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
 CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG 2400
 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGCGTACG 2460
 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGAATTCA TTGGGATGTT TCAGTTGA

28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTAAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...942
- (D) OTHER INFORMATION: Renilla Reiniformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
1 5 10 15

48

ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
20 25 30

96

CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
35 40 45

144

GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
50 55 60

192

CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
65 70 75 80

240

CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
85 90 95

288

| | |
|---|-----|
| TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile 100 105 110 | 336 |
| TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu 115 120 125 | 384 |
| GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val 130 135 140 | 432 |
| CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro 145 150 155 160 | 480 |
| GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys 165 170 175 | 528 |
| ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys 180 185 190 | 576 |
| ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro 195 200 205 | 624 |
| TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg 210 215 220 | 672 |
| GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val 225 230 235 240 | 720 |
| AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met 245 250 255 | 768 |
| TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly 260 265 270 | 816 |
| GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His 275 280 285 | 864 |
| TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser 290 295 300 | 912 |
| TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA Phe Val Glu Arg Val Leu Lys Asn Glu Gln 305 310 | 945 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTGGTCAC

30

09096518-095296